

What is claimed is:

1. A purified or isolated polypeptide that comprises an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence set forth in SEQ ID NO: 4;
 - (b) a fragment of (a) that exhibits aspartyl protease activity involved in processing APP into amyloid beta and includes aspartyl protease active site tripeptides DTG and DSG;
 - (c) a conservative substitution variant of (a) or (b) having an amino acid sequence identical to (a) or (b) except for conservative substitutions, wherein the conservative substitution variant comprises an amino acid sequence encoded by a nucleic acid molecule that hybridizes under the following stringent hybridization conditions to the complement of SEQ ID NO: 3:
 - (1) hybridization at 42°C in a hybridization buffer comprising 6x SSC and 0.1% SDS, and
 - (2) washing at 65°C in a wash solution comprising 1x SSC and 0.1% SDS;
- wherein the conservative substitution variant exhibits aspartyl protease activity involved in processing APP into amyloid beta.
2. A purified or isolated polypeptide that comprises an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence set forth in SEQ ID NO: 6;
 - (b) a fragment of (a) that exhibits aspartyl protease activity involved in processing APP into amyloid beta and includes aspartyl protease active site tripeptides DTG and DSG;
 - (c) a conservative substitution variant of (a) or (b) having an amino acid sequence identical to (a) or (b) except for conservative substitutions, wherein the conservative substitution variant comprises an amino acid sequence encoded by a nucleic acid molecule that hybridizes under the following stringent hybridization conditions to the complement of SEQ ID NO: 5:
 - (1) hybridization at 42°C in a hybridization buffer comprising 6x SSC and 0.1% SDS, and

(2) washing at 65°C in a wash solution comprising 1x SSC and 0.1% SDS;

wherein the conservative substitution variant exhibits aspartyl protease activity involved in processing APP into amyloid beta.

3. A purified or isolated polypeptide according to claim 1 or 2, further comprising a heterologous peptide tag.

4. A purified or isolated polypeptide according to claim 1 or 2, wherein the polypeptide lacks a transmembrane domain.

5. A purified or isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 1 or 2.

6. A method for identifying an agent that decreases the protease activity of an aspartyl protease polypeptide comprising steps of:

(a) expressing the aspartyl protease polypeptide of claim 1 or 2 by growing a host cell transformed or transfected with a polynucleotide that encodes the polypeptide, under conditions wherein the cell expresses the polypeptide encoded by the polynucleotide,

(b) measuring proteolytic activity of the polypeptide in the presence and absence of a test agent; and

(c) comparing proteolytic activity of the polypeptide in the presence and absence of the test agent, wherein decreased proteolytic activity in the presence of the test agent identifies the test agent as an agent that decreases the protease activity of the aspartyl protease polypeptide.

7. A method for identifying an agent that decreases the protease activity of an aspartyl protease polypeptide comprising steps of:

(a) expressing an aspartyl protease polypeptide by growing a host cell transformed or transfected with a polynucleotide in the presence and absence of a test agent; under conditions wherein the cell expresses the polypeptide encoded by the polynucleotide,

wherein the polynucleotide comprises a nucleotide sequence that hybridizes under the following stringent hybridization conditions to the complement of SEQ ID NO: 3 or SEQ ID NO: 5:

- (1) hybridization at 42°C in a hybridization buffer comprising 6x SSC and 0.1% SDS, and
- (2) washing at 65°C in a wash solution comprising 1x SSC and 0.1% SDS; wherein the polynucleotide encodes a polypeptide comprising a contiguous amino acid sequence that the aspartyl protease active site tripeptides DTG and DSG and exhibits aspartyl protease activity involved in processing APP into amyloid beta, wherein said polypeptide lacks a transmembrane domain, and wherein said polypeptide exhibits aspartyl protease activity involved in processing APP into amyloid beta

- (b) measuring proteolytic activity of said polypeptide in the presence and absence of a test agent; and
- (c) comparing proteolytic activity of the polypeptide in the presence and absence of the test agent, wherein decreased proteolytic activity in the presence of the test agent identifies the test agent as an agent that decreases the protease activity of the aspartyl protease polypeptide.

8. A method according to claim 6 or 7 wherein the proteolytic activity of steps (b) and (c) is proteolytic activity towards an APP substrate.

9. A method according to claim 8, wherein the APP substrate comprises an amyloid beta (A-beta) processing site.

10. A method according to claim 9, wherein the APP substrate comprises the Swedish mutation (K→N, M→L).

11. A method according to claim 9, wherein the APP substrate is a peptide comprising a β-secretase cleavage site that comprises the formula P2-P1-P1'-P2' (SEQ ID NO:74), wherein

P2 is an amino acid selected from K and N;

P1 is an amino acid selected from M and L;

P1' is the amino acid D; and

P2' is the amino acid A.

12. An isolated nucleic acid comprising nucleotides encoding a biologically active human aspartyl protease containing a valine at a position which corresponds to position 130 of SEQ ID NO:4, or a conservative substitute therefor, which isolated nucleic acid hybridizes under stringent wash conditions to a nucleic acid encoding the amino acid sequence set forth in SEQ ID NO: 4.

13. An isolated nucleic acid comprising nucleotides encoding a biologically active human aspartyl protease, the sequence of which isolated nucleic acid is identical to a sequence set forth within SEQ ID NO: 3.

14. A vector comprising the isolated nucleic acid of any one of claims 12 or 13.

15. A host cell comprising the vector of claim 14.

16. An isolated biologically active human aspartyl protease containing a valine at a position which corresponds to position 130 of SEQ ID NO:4, which human aspartyl protease is encoded by a nucleic acid which hybridizes under stringent wash conditions to a nucleic acid encoding the amino acid sequence set forth in SEQ ID NO: 4.

17. An isolated biologically active human aspartyl protease containing a valine at a position which corresponds to position 130 of SEQ ID NO: 4, which human aspartyl protease is encoded by a nucleic acid which is identical across its length to the sequence set forth in SEQ ID NO: 3.

18. An isolated biologically active human aspartyl protease containing a valine at a position which corresponds to position 130 of SEQ ID NO: 4, which human aspartyl protease is encoded by a nucleic acid which is identical to a sequence set forth within SEQ ID NO: 3.

19. An isolated polypeptide with aspartyl protease activity comprising an amino acid sequence which is identical across its length to a sequence in SEQ ID NO: 4.

20. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide with aspartyl protease activity, wherein said polypeptide comprises an amino acid sequence which is identical across its length to a sequence in SEQ ID NO: 4.